



OIPE

## RAW SEQUENCE LISTING

DATE: 07/08/2002

PATENT APPLICATION: US/10/077,745

TIME: 10:07:43

Input Set : A:\PTO.PG.txt

Output Set: N:\CRF3\07082002\J077745.raw

3 <110> APPLICANT: KODA, TAKAYUKI  
 4 SATO, KAZUHIRO  
 6 <120> TITLE OF INVENTION: ORGANIC NITROGEN-CONTAINING COMPOSITION AND FERTILIZER  
 COMPRISING THE  
 7 SAME  
 9 <130> FILE REFERENCE: 219843US0  
 11 <140> CURRENT APPLICATION NUMBER: 10/077,745  
 12 <141> CURRENT FILING DATE: 2002-02-20  
 14 <150> PRIOR APPLICATION NUMBER: JP 2001-044137  
 15 <151> PRIOR FILING DATE: 2001-02-20  
 17 <160> NUMBER OF SEQ ID NOS: 8  
 19 <170> SOFTWARE: PatentIn version 3.1  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 935  
 23 <212> TYPE: PRT  
 24 <213> ORGANISM: Enterobacter agglomerans  
 26 <400> SEQUENCE: 1  
 28 Met Gln Asn Ser Ala Met Lys Pro Trp Leu Asp Ser Ser Trp Leu Ala  
 29 1 5 10 15  
 32 Gly Ala Asn Gln Ser Tyr Ile Glu Gln Leu Tyr Glu Asp Phe Leu Thr  
 33 20 25 30  
 36 Asp Pro Asp Ser Val Asp Ala Val Trp Arg Ser Met Phe Gln Gln Leu  
 37 35 40 45  
 40 Pro Gly Thr Gly Val Lys Pro Glu Gln Phe His Ser Ala Thr Arg Glu  
 41 50 55 60  
 44 Tyr Phe Arg Arg Leu Ala Lys Asp Ala Ser Arg Tyr Thr Ser Ser Val  
 45 65 70 75 80  
 48 Thr Asp Pro Ala Thr Asn Ser Lys Gln Val Lys Val Leu Gln Leu Ile  
 49 85 90 95  
 52 Asn Ala Phe Arg Phe Arg Gly His Gln Glu Ala Asn Leu Asp Pro Leu  
 53 100 105 110  
 56 Gly Leu Trp Lys Gln Asp Arg Val Ala Asp Leu Asp Pro Ala Phe His  
 57 115 120 125  
 60 Asp Leu Thr Asp Ala Asp Phe Gln Glu Ser Phe Asn Val Gly Ser Phe  
 61 130 135 140  
 64 Ala Ile Gly Lys Glu Thr Met Lys Leu Ala Asp Leu Phe Asp Ala Leu  
 65 145 150 155 160  
 68 Lys Gln Thr Tyr Cys Gly Ser Ile Gly Ala Glu Tyr Met His Ile Asn  
 69 165 170 175  
 72 Asn Thr Glu Glu Lys Arg Trp Ile Gln Gln Arg Ile Glu Ser Gly Ala  
 73 180 185 190  
 76 Ser Gln Thr Ser Phe Ser Gly Glu Glu Lys Lys Gly Phe Leu Lys Glu  
 77 195 200 205  
 80 Leu Thr Ala Ala Glu Gly Leu Glu Lys Tyr Leu Gly Ala Lys Phe Pro

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81      210      215      220
84 Gly Ala Lys Arg Phe Ser Leu Glu Gly Gly Asp Ala Leu Val Pro Met
85 225      230      235      240
88 Leu Arg Glu Met Ile Arg His Ala Gly Lys Ser Gly Thr Arg Glu Val
89      245      250      255
92 Val Leu Gly Met Ala His Arg Gly Arg Leu Asn Val Leu Ile Asn Val
93      260      265      270
96 Leu Gly Lys Lys Pro Gln Asp Leu Phe Asp Glu Phe Ser Gly Lys His
97      275      280      285
100 Lys Glu His Leu Gly Thr Gly Asp Val Lys Tyr His Met Gly Phe Ser
101      290      295      300
104 Ser Asp Ile Glu Thr Glu Gly Gly Leu Val His Leu Ala Leu Ala Phe
105 305      310      315      320
108 Asn Pro Ser His Leu Glu Ile Val Ser Pro Val Val Met Gly Ser Val
109      325      330      335
112 Arg Ala Arg Leu Asp Arg Leu Ala Glu Pro Val Ser Asn Lys Val Leu
113      340      345      350
116 Pro Ile Thr Ile His Gly Asp Ala Ala Val Ile Gly Gln Gly Val Val
117      355      360      365
120 Gln Glu Thr Leu Asn Met Ser Gln Ala Arg Gly Tyr Glu Val Gly Gly
121      370      375      380
124 Thr Val Arg Ile Val Ile Asn Asn Gln Val Gly Phe Thr Thr Ser Asn
125 385      390      395      400
128 Pro Lys Asp Ala Arg Ser Thr Pro Tyr Cys Thr Asp Ile Gly Lys Met
129      405      410      415
132 Val Leu Ala Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala Val
133      420      425      430
136 Ala Phe Val Thr Arg Leu Ala Leu Asp Tyr Arg Asn Thr Phe Lys Arg
137      435      440      445
140 Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Arg His Gly His Asn Glu
141      450      455      460
144 Ala Asp Glu Pro Ser Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys
145 465      470      475      480
148 Lys His Pro Thr Pro Arg Lys Ile Tyr Ala Asp Arg Leu Glu Gly Glu
149      485      490      495
152 Gly Val Ala Ser Gln Glu Asp Ala Thr Glu Met Val Asn Leu Tyr Arg
153      500      505      510
156 Asp Ala Leu Asp Ala Gly Glu Cys Val Val Pro Glu Trp Arg Pro Met
157      515      520      525
160 Ser Leu His Ser Phe Thr Trp Ser Pro Tyr Leu Asn His Glu Trp Asp
161      530      535      540
164 Glu Pro Tyr Pro Ala Gln Val Asp Met Lys Arg Leu Lys Glu Leu Ala
165 545      550      555      560
168 Leu Arg Ile Ser Gln Val Pro Glu Gln Ile Glu Val Gln Ser Arg Val
169      565      570      575
172 Ala Lys Ile Tyr Asn Asp Arg Lys Leu Met Ala Glu Gly Glu Lys Ala
173      580      585      590
176 Phe Asp Trp Gly Gly Ala Glu Asn Leu Ala Tyr Ala Thr Leu Val Asp
177      595      600      605

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180 Glu Gly Ile Pro Val Arg Leu Ser Gly Glu Asp Ser Gly Arg Gly Thr
181      610      615      620
184 Phe Phe His Arg His Ala Val Val His Asn Gln Ala Asn Gly Ser Thr
185 625      630      635      640
188 Tyr Thr Pro Leu His His Ile His Asn Ser Gln Gly Glu Phe Lys Val
189      645      650      655
192 Trp Asp Ser Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly
193      660      665      670
196 Tyr Ala Thr Ala Glu Pro Arg Val Leu Thr Ile Trp Glu Ala Gln Phe
197      675      680      685
200 Gly Asp Phe Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser
201      690      695      700
204 Ser Gly Glu Gln Lys Trp Gly Arg Met Cys Gly Leu Val Met Leu Leu
205 705      710      715      720
208 Pro His Gly Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu
209      725      730      735
212 Glu Arg Tyr Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Cys Val
213      740      745      750
216 Pro Ser Thr Pro Ala Gln Val Tyr His Met Leu Arg Arg Gln Ala Leu
217      755      760      765
220 Arg Gly Met Arg Arg Pro Leu Val Val Met Ser Pro Lys Ser Leu Leu
221      770      775      780
224 Arg His Pro Leu Ala Ile Ser Ser Leu Asp Glu Leu Ala Asn Gly Ser
225 785      790      795      800
228 Phe Gln Pro Ala Ile Gly Glu Ile Asp Asp Leu Asp Pro Gln Gly Val
229      805      810      815
232 Lys Arg Val Val Leu Cys Ser Gly Lys Val Tyr Tyr Asp Leu Leu Glu
233      820      825      830
236 Gln Arg Arg Lys Asp Glu Lys Thr Asp Val Ala Ile Val Arg Ile Glu
237      835      840      845
240 Gln Leu Tyr Pro Phe Pro His Gln Ala Val Gln Glu Ala Leu Lys Ala
241      850      855      860
244 Tyr Ser His Val Gln Asp Phe Val Trp Cys Gln Glu Glu Pro Leu Asn
245 865      870      875      880
248 Gln Gly Ala Trp Tyr Cys Ser Gln His His Phe Arg Asp Val Val Pro
249      885      890      895
252 Phe Gly Ala Thr Leu Arg Tyr Ala Gly Arg Pro Ala Ser Ala Ser Pro
253      900      905      910
256 Ala Val Gly Tyr Met Ser Val His Gln Gln Gln Gln Gln Asp Leu Val
257      915      920      925
260 Asn Asp Ala Leu Asn Val Asn
261      930      935
264 <210> SEQ ID NO: 2
265 <211> LENGTH: 407
266 <212> TYPE: PRT
267 <213> ORGANISM: Enterobacter agglomerans
269 <400> SEQUENCE: 2
271 Met Ser Ser Val Asp Ile Leu Val Pro Asp Leu Pro Glu Ser Val Ala
272 1      5      10      15

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275 Asp Ala Thr Val Ala Thr Trp His Lys Lys Pro Gly Asp Ala Val Ser
276          20          25          30
279 Arg Asp Glu Val Ile Val Glu Ile Glu Thr Asp Lys Val Val Leu Glu
280          35          40          45
283 Val Pro Ala Ser Ala Asp Gly Val Leu Glu Ala Val Leu Glu Asp Glu
284          50          55          60
287 Gly Ala Thr Val Thr Ser Arg Gln Ile Leu Gly Arg Leu Lys Glu Gly
288 65          70          75          80
291 Asn Ser Ala Gly Lys Glu Ser Ser Ala Lys Ala Glu Ser Asn Asp Thr
292          85          90          95
295 Thr Pro Ala Gln Arg Gln Thr Ala Ser Leu Glu Glu Glu Ser Ser Asp
296          100         105         110
299 Ala Leu Ser Pro Ala Ile Arg Arg Leu Ile Ala Glu His Asn Leu Asp
300          115         120         125
303 Ala Ala Gln Ile Lys Gly Thr Gly Val Gly Gly Arg Leu Thr Arg Glu
304          130         135         140
307 Asp Val Glu Lys His Leu Ala Asn Lys Pro Gln Ala Glu Lys Ala Ala
308 145          150         155         160
311 Ala Pro Ala Ala Gly Ala Ala Thr Ala Gln Gln Pro Val Ala Asn Arg
312          165         170         175
315 Ser Glu Lys Arg Val Pro Met Thr Arg Leu Arg Lys Arg Val Ala Glu
316          180         185         190
319 Arg Leu Leu Glu Ala Lys Asn Ser Thr Ala Met Leu Thr Thr Phe Asn
320          195         200         205
323 Glu Ile Asn Met Lys Pro Ile Met Asp Leu Arg Lys Gln Tyr Gly Asp
324          210         215         220
327 Ala Phe Glu Lys Arg His Gly Val Arg Leu Gly Phe Met Ser Phe Tyr
328 225          230         235         240
331 Ile Lys Ala Val Val Glu Ala Leu Lys Arg Tyr Pro Glu Val Asn Ala
332          245         250         255
335 Ser Ile Asp Gly Glu Asp Val Val Tyr His Asn Tyr Phe Asp Val Ser
336          260         265         270
339 Ile Ala Val Ser Thr Pro Arg Gly Leu Val Thr Pro Val Leu Arg Asp
340          275         280         285
343 Val Asp Ala Leu Ser Met Ala Asp Ile Glu Lys Lys Ile Lys Glu Leu
344          290         295         300
347 Ala Val Lys Gly Arg Asp Gly Lys Leu Thr Val Asp Asp Leu Thr Gly
348 305          310         315         320
351 Gly Asn Phe Thr Ile Thr Asn Gly Gly Val Phe Gly Ser Leu Met Ser
352          325         330         335
355 Thr Pro Ile Ile Asn Pro Pro Gln Ser Ala Ile Leu Gly Met His Ala
356          340         345         350
359 Ile Lys Asp Arg Pro Met Ala Val Asn Gly Gln Val Val Ile Leu Pro
360          355         360         365
363 Met Met Tyr Leu Ala Leu Ser Tyr Asp His Arg Leu Ile Asp Gly Arg
364          370         375         380
367 Glu Ser Val Gly Tyr Leu Val Ala Val Lys Glu Met Leu Glu Asp Pro
368 385          390         395         400
371 Ala Arg Leu Leu Leu Asp Val

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372                               405
375 <210> SEQ ID NO: 3
376 <211> LENGTH: 41
377 <212> TYPE: PRT
378 <213> ORGANISM: Enterobacter agglomerans
380 <400> SEQUENCE: 3
382 Met Asn Leu His Glu Tyr Gln Ala Lys Gln Leu Phe Ala Arg Tyr Gly
383 1                               5                               10                               15
386 Met Pro Ala Pro Thr Gly Tyr Ala Cys Thr Thr Pro Arg Glu Ala Glu
387                               20                               25                               30
390 Glu Ala Ala Ser Lys Ile Gly Ala Gly
391                               35                               40
394 <210> SEQ ID NO: 4
395 <211> LENGTH: 39
396 <212> TYPE: PRT
397 <213> ORGANISM: Enterobacter agglomerans
399 <400> SEQUENCE: 4
401 Ala Phe Ser Val Phe Arg Cys His Ser Ile Met Asn Cys Val Ser Val
402 1                               5                               10                               15
405 Cys Pro Lys Gly Leu Asn Pro Thr Arg Ala Ile Gly His Ile Lys Ser
406                               20                               25                               30
409 Met Leu Leu Gln Arg Ser Ala
410                               35
413 <210> SEQ ID NO: 5
414 <211> LENGTH: 933
415 <212> TYPE: PRT
416 <213> ORGANISM: Escherichia coli
418 <400> SEQUENCE: 5
420 Met Gln Asn Ser Ala Leu Lys Ala Trp Leu Asp Ser Ser Tyr Leu Ser
421 1                               5                               10                               15
424 Gly Ala Asn Gln Ser Trp Ile Glu Gln Leu Tyr Glu Asp Phe Leu Thr
425                               20                               25                               30
428 Asp Pro Asp Ser Val Asp Ala Asn Trp Arg Ser Thr Phe Gln Gln Leu
429                               35                               40                               45
432 Pro Gly Thr Gly Val Lys Pro Asp Gln Phe His Ser Gln Thr Arg Glu
433                               50                               55                               60
436 Tyr Phe Arg Arg Leu Ala Lys Asp Ala Ser Arg Tyr Ser Ser Thr Ile
437 65                               70                               75                               80
440 Ser Asp Pro Asp Thr Asn Val Lys Gln Val Lys Val Leu Gln Leu Ile
441                               85                               90                               95
444 Asn Ala Tyr Arg Phe Arg Gly His Gln His Ala Asn Leu Asp Pro Leu
445                               100                              105                              110
448 Gly Leu Trp Gln Gln Asp Lys Val Ala Asp Leu Asp Pro Ser Phe His
449                               115                              120                              125
452 Asp Leu Thr Glu Ala Asp Phe Gln Glu Thr Phe Asn Val Gly Ser Phe
453                               130                              135                              140
456 Ala Ser Gly Lys Glu Thr Met Lys Leu Gly Glu Leu Leu Glu Ala Leu
457 145                              150                              155                              160
460 Lys Gln Thr Tyr Cys Gly Pro Ile Gly Ala Glu Tyr Met His Ile Thr

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VERIFICATION SUMMARY

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